

**BLAST****Basic Local Alignment Search Tool**

- Your search parameters were adjusted to search for a short input sequence.

[Edit](#) and Resubmit [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)**Protein Sequence (15 letters)**

residues 66-80 of SEQ ID NO: 12

Results for: ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**  
**Description**

None

**Molecule type**

amino acid

**Query Length**

15

**Database Name**

nr

**Description**

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

**Program**BLASTP 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#) [NEW](#)

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**Search Parameters**

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

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**Database**

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.358076	0.294
K	0.289736	0.11
H	1.81294	0.61

### Results Statistics

Length adjustment 5  
Effective length of query 10  
Effective length of database 3454422147  
Effective search space 34544221470  
Effective search space used 34544221470

Graphic Summary

Show Conserved Domains

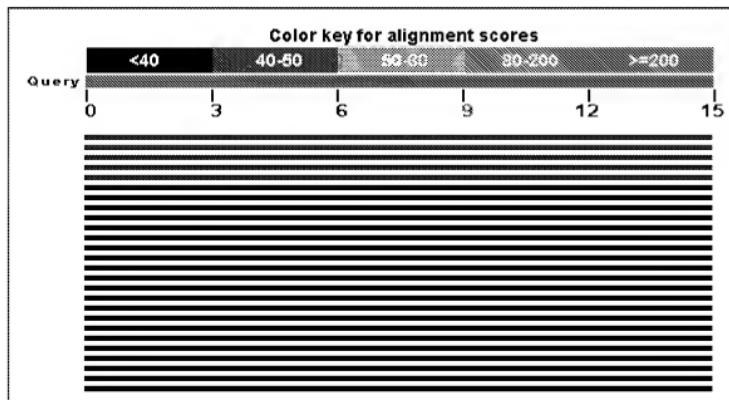
No putative conserved domains have been detected

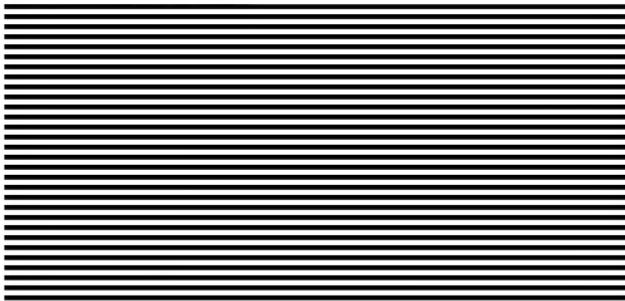


### Distribution of 100 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





The image shows a large rectangular area filled with horizontal black bars, representing a redacted protein sequence. The bars are evenly spaced and extend across the width of the redacted area.

## Descriptions

		Score
E	Sequences producing significant alignments:	(Bits) Value
gb ABU97133.11	S protein [Hepatitis B virus]	43.5 0.003
gb ABU9712005.11	surface antigen [Hepatitis B virus]	43.5 0.003
gb JARH12008.11	S protein [Hepatitis B virus]	43.5 0.003
gb JARH12008.11	HBSAg [Hepatitis B virus]	43.5 0.003
gb ARDL3661.11	surface antigen [Hepatitis B virus]	42.2 0.007
gb ACX36965.11	middle S protein [Hepatitis B virus] >gb ACX36...	39.7 0.040
gb ACX36957.11	middle S protein [Hepatitis B virus]	39.7 0.040
gb JARH07446.11	hepatitis B surface antigen [Hepatitis B virus]	39.7 0.040
gb ACQ83792.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACQ82751.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACQ82750.11	large S protein [Hepatitis B virus]	38.8 0.072
gb EAR04154.11	hepatitis B surface antigen [Hepatitis B virus]	38.8 0.072
gb JARH4107.11	hepatitis B surface antigen [Hepatitis B virus]	38.8 0.072
gb JARH3939.11	hepatitis B surface antigen [Hepatitis B virus]	38.8 0.072
gb ACJ66248.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66247.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66242.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66241.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66240.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66233.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66232.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66227.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66226.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66225.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66212.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66207.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66205.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66205.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66164.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66165.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66136.11	middle S protein [Hepatitis B virus] >gb ACJ66...	38.8 0.072
gb ACJ66135.11	large S protein [Hepatitis B virus] >gb ACJ661...	38.8 0.072
gb ACJ66130.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66129.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66128.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66127.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66095.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66095.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66094.11	large S protein [Hepatitis B virus] >gb ACJ660...	38.8 0.072
gb ACJ66006.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66005.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ66004.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ65907.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ65906.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACJ65858.11	S protein [Hepatitis B virus]	38.8 0.072
gb ACJ65858.11	middle S protein [Hepatitis B virus]	38.8 0.072
gb ACJ65857.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66198.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66193.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66192.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66180.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66179.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66169.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACR66122.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACP66138.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACP66129.11	large S protein [Hepatitis B virus]	38.8 0.072
gb ACP66128.11	large S protein [Hepatitis B virus]	38.8 0.072

gb ACR66997.11	large S protein [Hepatitis B virus]	>gb ACR661...	38.8	0.072
gb ACR66998.11	large S protein [Hepatitis B virus]		38.9	0.072
gb ACR66996.11	large S protein [Hepatitis B virus]		38.9	0.072
gb ACR66990.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR66991.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65984.11	large S protein [Hepatitis B virus]	>gb ACR661...	38.8	0.072
gb ACP65244.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65243.11	large S protein [Hepatitis B virus]	>gb ACR659...	38.8	0.072
gb ACP65241.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65222.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65223.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65920.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65903.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65891.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65894.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65889.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACP65878.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65869.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65859.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65855.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65852.11	large S protein [Hepatitis B virus]	>gb ACR659...	38.8	0.072
gb ACR65840.11	large S protein [Hepatitis B virus]	>gb ACR660...	38.8	0.072
gb ACR65833.11	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACR65825.11	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACR65517.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACR65809.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP65807.11	large S protein [Hepatitis B virus]	>gb ACR658...	38.8	0.072
gb ACR20194.11	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20193.11	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20790.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20564.11	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20563.11	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20560.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20153.11	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20412.11	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20411.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20326.11	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20325.11	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACF20324.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20320.11	S protein [Hepatitis B virus]		38.8	0.072
gb ACP20319.11	middle S protein [Hepatitis B virus]		38.8	0.072
gb ACP20318.11	large S protein [Hepatitis B virus]		38.8	0.072
gb ACP20311.11	S protein [Hepatitis B virus]		38.8	0.072

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>gb|ABU97123.1| S protein [Hepatitis B virus]  
Length=57

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGCK 15  
Sbjct 1 PLIPGST TSTGCK 15

>gb|ABI17005.1| surface antigen [Hepatitis B virus]  
Length=57

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGCK 15  
Sbjct 1 PLIPGST TSTGCK

Sbjct 1 PLIPGSTTTSTGQCK 15

>dbj|BAG12008.1| S protein [Hepatitis B virus]  
Length=254

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTGQCK  
Sbjct 136 PLIPGSTTTSTGQCK 150

>gb|AAW65562.1| HBsAg [Hepatitis B virus]  
Length=226

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTGQCK  
Sbjct 108 PLIPGSTTTSTGQCK 122

>gb|AAD13661.1| surface antigen [Hepatitis B virus]  
Length=226

Score = 42.2 bits (92), Expect = 0.007  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPG+TRTSTG CK  
Sbjct 108 PLIPGTTTSTGPCK 122

>gb|ACX36965.1| middle S protein [Hepatitis B virus]  
>gb|ACX36975.1| middle S protein [Hepatitis B virus]  
Length=243

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PL+PGST TSTGQCK  
Sbjct 125 PLLPGSTTTSTGQCK 139

>gb|ACX36957.1| middle S protein [Hepatitis B virus]  
Length=243

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PL+PGST TSTGQCK  
Sbjct 125 PLLPGSTTTSTGQCK 139

>dbj|BAG06746.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGTTTSTGXCK 83

>gb|ACQ82752.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGTTTSTGPCK 122

>gb|ACQ82751.1| middle S protein [Hepatitis B virus]  
Length=281  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACQ82750.1| large S protein [Hepatitis B virus]  
Length=400  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>dbj|BAH84154.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTSTGPCK 83

>dbj|BAH84102.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTSTGPCK 83

>dbj|BAH83930.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTSTGPCK 83

>gb|ACJ66248.1| middle S protein [Hepatitis B virus]  
Length=281  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66247.1| large S protein [Hepatitis B virus]  
Length=400  
Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)  
Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66242.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 108 PLIPGST TSTG CK 122

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 163 PLIPGST TSTG CK 177

>gb|ACJ66240.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 282 PLIPGST TSTG CK 296

>gb|ACJ66233.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 282 PLIPGST TSTG CK 296

>gb|ACJ66228.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 108 PLIPGST TSTG CK 122

>gb|ACJ66227.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 163 PLIPGST TSTG CK 177

>gb|ACJ66226.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
Sbjct 282 PLIPGST TSTG CK 296

>gb|ACJ66213.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66212.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66207.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66206.1| middle S protein [Hepatitis B virus]  
Length=279

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 161 PLIPGSTTTSTGPCK 175

>gb|ACJ66205.1| large S protein [Hepatitis B virus]  
Length=398

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 280 PLIPGSTTTSTGPCK 294

>gb|ACJ66164.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66163.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66136.1| middle S protein [Hepatitis B virus]  
gb|ACJ66178.1| middle S protein [Hepatitis B virus]  
gb|ACJ66192.1| middle S protein [Hepatitis B virus]  
gb|ACJ66198.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66135.1| large S protein [Hepatitis B virus]  
gb|ACJ66177.1| large S protein [Hepatitis B virus]  
gb|ACJ66191.1| large S protein [Hepatitis B virus]  
gb|ACJ66203.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66130.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66129.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66128.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66122.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66096.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66095.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66081.1| large S protein [Hepatitis B virus]  
gb|ACJ66088.1| large S protein [Hepatitis B virus]  
gb|ACJ66142.1| large S protein [Hepatitis B virus]  
gb|ACJ66156.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66006.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66005.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66004.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ65907.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ65906.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ65859.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ65858.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ65857.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACR66198.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66183.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66182.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66180.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66170.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTG CK

Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66160.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66152.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66138.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66129.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66123.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66097.1| large S protein [Hepatitis B virus]  
>gb|ACR66110.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66094.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRSTGQCK 15  
PLIPGST TSTG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134